

Fig. 1A

GAAGCAAGGAGGCGGCGGCGGCCGAGCGAGTGGCGAGTAGTGGAACGTTGC
 TTCTGAGGGGAGCCCAAGATGACCGGTTCTAACGAGTTCAAGCTGAACCAGCC
 ACCCGAGGATGGCATCTCCTCCGTGAAGTTCAGCCCCAACACCTCCAGTTCCT
 GCTTGTCTCCTCCTGGGACACGTCCGTGCGTCTCTACGATGTGCCGGCCAACTCC
 ATGCGGCTCAAGTACCAGCACACCGGCGCCGTCTGGACTGCGCCTTCTACGAT
 CCAACGCATGCCTGGAGTGGAGGACTAGATCATCAATTGAAAATGCATGATT
 TGAACACTGATCAAGAAAATCTTGTTGGGACCCATGATGCCCCTATCAGATGT
 GTTGAATACTGTCCAGAAGTGAATGTGATGGTCACTGGAAGTTGGGATCAGA
 CAGTTAACTGTGGGATCCCAGAACTCCTTGTAATGCTGGGACCTTCTCTCAGC
 CTGAAAAGGTATATACCCTCTCAGTGTCTGGAGACCGGCTGATTGTGGGAACA
 GCAGGCCGCAGAGTGTTGGTGTGGGACTTACGGAACATGGGTTACGTGCAGCA
 GCGCAGGGAGTCCAGCCTGAAATACCAGACTCGCTGCATACGAGCGTTTCCAA
 ACAAGCAGGGTTATGTATTAAGCTCTATTGAAGGCCGAGTGGCAGTTGAGTA
 TTTGGACCCAAGCCCTGAGGTACAGAAGAAGAAGTATGCCCTCAAATGTCAC
 AGACTAAAAGAAAATAATATTGAGCAGATTTACCCAGTCAATGCCATTTCTT
 TTCACAATATCCACAATACATTTGCCACAGGTGGTTCTGATGGCTTTGTAAAT
 ATTTGGGATCCATTTAACAAAAAGCGACTGTGCCAATTCATCGGTACCCAC
 GAGCATCGCATCACTTGCCTTCAGTAATGATGGGACTACGCTTGCAATAGCGT
 CATCATATATGTATGAAATGGATGACACAGAACATCCTGAAGATGGTATCTT
 CATTCGCCAAGTGACAGATGCAGAAACAAAACCCAGTCACCATGTACTGA
 CAAGATTTCACTTAAAGTGCCATGTTGATGATAATAAAACAATTCGTAC
 TCCCCAATGGTGGATTTATTACTATTAAGAAACCAGGGAAAATATTAATTT
 TAATATTATAACAACCTGAAAATAATGGAAAAGAGTTTTTGAATTTTTTTT
 TTTAAATAAACACCTTCTTAAGTGCATGAGATGGTTTGATGGTTTGCTGCATT
 AAAGGTATTTGGGCAAACAAAATTGGAGGGCAAGTGACTGCAGTTTGGAGA
 ATCAGTTTTGACCTTGATGATTTTTTGTTCCTGTGGAAATAAATGTTTGTA
 AATAAGTGTAATAAAAAATCCCTTGCATTCTTCTGGACCTTAAATGGTAGA
 GGAAAAGGCTCGTGAGCCATTTGTTTCTTTTGCTGGTTATAGTTGCTAATTCTA
 AAGCTGCTTCAGACTGCTTCATGAGGAGGTTAATCTACAATTAACAATATT
 TCCTCTTGGCCGTCCATTATTTTCTGAAGCAGATGGTTCATCATTTCTGGGCTG
 TTAACAAAGCGAGGTTAAGGTTAGACTCTTGGGAATCAGCTAGTTTTCAAT
 CTTATTAGGGTGCAGAAGGAAAATAATAAGAAAACCTCCTAATATCATTTT
 GTGACTGTAAACAATTATTTATTAGCAAACAATTGATCCAGAAGGGCAAAT
 TGTTTGAGTCAGTAATGAGCTGAGAAAAGACAGAGCATATCTGTGATTTGG
 AAAAAATAATTGTAACGTAATTGCAGTGCATTTAGACAGGCATCTATTTGGAC
 CTGTTTCTATCTCTAAATGAATTTTTGGAAACATTAATGAGGTTTACATATTT
 CTCTGACATTTATATAGTTCTTATGTCCATTTAGTTGACCAGCCGCTGGTGAT
 TAAAGTTAAAAGAAAAAATTATAGTGAGAATGAGATTCATTTCAATGTA
 ATGCACTAAAGCAGAACACGAACCTTAGCTTGGCCTATTCTAGGTAGTTCCAA
 ATAGTATTTTGTGTCAAACCTTTAAATTTATATTAATTTGCAAATGTATGT
 CTCTGAGTAGGACTTGGACCTTCTCTGAGATTTATTTTATCCGTGATGTATTTT
 TTTTAATTTCTTTTGATACAGAGAAGGGCTTTTTTTTTTTAAGTATTTCAAGTGA
 AAACCTGGTGTAAGTCTGAACCCATCTTTGAAATGTATTTCTTCATTGCAG

Fig. 1B

GTCCACCTAATCATCCTGTGAAAGTGGTTTCTCTATGGAAAGCTTTGTTTGCTT
 CCTACAAATACATGCTTATTCCTTAAGGGATGTGTTAGAGTTACTGTGGATTT
 CTCTGTTTTCTGTCTTACAAGAACTTGTCTATGTACCTTAATACTTTGTTTAG
 GATGAGGAGTCTTTGTGTCCCTGTACAGTAGTCTGACGTATTTCCCCTTCTGTC
 CCCTAGTAAGCCCAGTTGCTGTATCTGAACAGTTTGAGCTCTTTTGTAAATATA
 CTCTAAACCTGTTATTTCTGTGCTAATAAACGAGATGCAGAACCCCTGAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Fig. 1B
 (Continued)

Alignment of predicted *huBUB3* gene products from ~1.4 Kb cDNA and ~2.7 Kb cDNA

| | | | |
|------------|--|-----|-----|
| | 20 | 40 | 60 |
| huBUB3 2.7 | MTGSNEFKLNQPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVL | | |
| huBUB3 1.4 | MTGSNEFKLNQPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVL | | |
| | 80 | 100 | 120 |
| huBUB3 2.7 | DCAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNMVMTGSWDQTV | | |
| huBUB3 1.4 | DCAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNMVMTGSWDQTV | | |
| | 140 | 160 | 180 |
| huBUB3 2.7 | KLWDPRTPCNAGTFSQPEKVYTLVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKY | | |
| huBUB3 1.4 | KLWDPRTPCNAGTFSQPEKVYTLVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKY | | |
| | 200 | 220 | 240 |
| huBUB3 2.7 | QTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAI | | |
| huBUB3 1.4 | QTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAI | | |
| | 260 | 280 | 300 |
| huBUB3 2.7 | SFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSYME | | |
| huBUB3 1.4 | SFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSYME | | |
| | 320 | | |
| huBUB3 2.7 | MDDTEHPEDGIFIRQVTDAETKPKSPCT | | |
| huBUB3 1.4 | MDDTEHPEDGIFIRQVTDAETKPKVHLIIL | | |

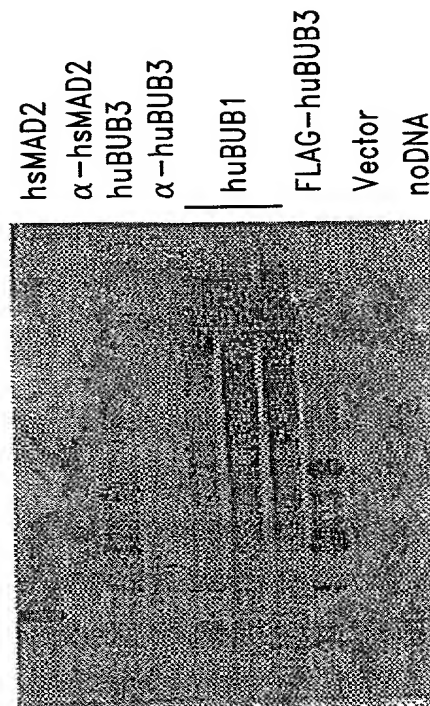
Fig. 2

| | | | |
|---------|-----|--|-----|
| scBUB3 | 1 | -----MQIVQIEQAPKDYISDIKIIP---SKSLLL | 27 |
| muBUB3 | 1 | -----MTG-----SNEFKLNQPPEDGISSVKFSPN--TSQFLL | 31 |
| huBUB3 | 1 | -----MTG-----SNEFKLNQPPEDGISSVKFSPN--TSQFLL | 31 |
| rae1-hu | 1 | MSLFGTTSFGTSGTSMFGSATT--DNHNPMKDIEVTSSPDDSIGCLSFSPPTLPGNFLI | 58 |
| rae1 | 1 | MSLFG-----QATTSTVSNATG-----DLKKDVEVAQPPEDSISDLAFSP---QAEYLA | 46 |
| yet7 | 1 | MSFFNR-----SNTTSALGTSTAMANEKDLANDIVINSPAEDSISDIAFSP---QQDFMF | 52 |
| | | . D I . P | |
| scBUB3 | 28 | -----I-----II----- -ITSWDGSLTVYKFDIQAKNVDLLQSLRYKH--PLLCCNFI-DNTDLQIYVGTVOGEILK | 83 |
| muBUB3 | 32 | -VSSWDT--SVRLYDVPA--NSM-R-LKYQHTGAVLDCAFY-DPT--HAWSGGLDHQLKM | 81 |
| huBUB3 | 32 | -VSSWDT--SVRLYDVPA--NSM-R-LKYQHTGAVLDCAFY-DPT--HAWSGGLDHQLKM | 81 |
| rae1-hu | 59 | -AGSWAN--DVRCEVQDSGQTI PK-AQQMHTGPVLDVCWSDDGS--KVFTASCDKTAKM | 112 |
| rae1 | 47 | -ASSWDS--KVRIYEVQATGQSIGK-ALYEHQGPVLSVNWSRDGT--KVASGSVDKSAKV | 100 |
| yet7 | 53 | SASSWDG--KVRIWDVQN-GVPQGR-AQHESSPVLC TRWSNDGT--KVASGGCDNALKL | 106 |
| | | SW VL D . . | |
| scBUB3 | 84 | -----III----- VDLIGSPSFQALTNNEANLGICRICKYGD--DKLIAASWDGLIEVIDPRNYGDGVI AVKN | 141 |
| muBUB3 | 82 | HDLNTDQENLVGTHDAPIRCVEYCEPVNV---MVTGSWDQTVKLWDPR-TPCNAGTFS- | 135 |
| huBUB3 | 82 | HDLNTDQENLVGTHDAPIRCVEYCEPVNV---MVTGSWDQTVKLWDPR-TPCNAGTFS- | 135 |
| rae1-hu | 113 | WDLSSNQAIQIAQHDAVPKTIHWIKAPNY--SCVMTGSWDKTLKFWDTIR-SSNPMMVLQ- | 168 |
| rae1 | 101 | FDIQTGQNNQVAAHDDAVRCVRFVEAMGT-SPI LATGSWDKTLKYWDLR-QSTPIATVS- | 157 |
| yet7 | 107 | YDIASGQTQQIGMHSAPIKVLRFVQCGPSNTECIVTGSWDKTIKYWDMR-QPQPSTVM- | 164 |
| | | D.SWD . D R | |
| scBUB3 | 142 | -----IV----- LNSNNTKVKNKIFTMDTNSSRLIVGMNNSQVQWFRPLCEDDNGTIEESGLKYQIRDVAL | 201 |
| muBUB3 | 136 | Q-----PEKVYTL SVSGDRLIVGTAGRRVLVWDLNMGYVQQRRE-SSLKYQTRCIRA | 187 |
| huBUB3 | 136 | Q-----PEKVYTL SVSGDRLIVGTAGRRVLVWDLNMGYVQQRRE-SSLKYQTRCIRA | 187 |
| rae1-hu | 169 | L-----PERCYCADVIYPMAVVATAERGLIVYQLENQPSEFRRIE-SPLKHQHRCAI | 220 |
| rae1 | 158 | L-----PERVYAMDCVHPLLTVATAERNICVINLSEPTKIFKLAM-SPLKFQTRSLAC | 209 |
| yet7 | 165 | M-----PERVYSMDNKQSLLVATAERHIAIINLANPTTIFKATT-SPLKWQTRCVAC | 216 |
| | | . . . V . L S L K Q R . | |

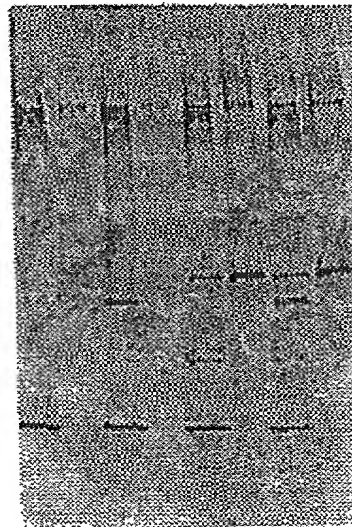
Fig. 3A

| | | | | |
|---------|-----|---|----------------|--|
| | | V | | |
| scBUB3 | 202 | LP---KEQEGYACSSIDGRVAVEFFDDQGDYNSKRFAFRCHRLNLKD-TNL----- | 250 | |
| muBUB3 | 188 | FP---NK-QGYVLSSIEGRVAVEYLDPS-PEV-QKKKYAFKCHRLKENN-IEQ----- | 233 | |
| huBUB3 | 188 | FP---NK-QGYVLSSIEGRVAVEYLDPS-PEV-QKKKYAFKCHRLKENN-IEQ----- | 233 | |
| rae1-hu | 221 | FKDKQNKPTGFALGSIEGRVAIHYNPP-NP--AKDNFTFKCHRSNGTNTSAP-----QD | 272 | |
| rae1 | 210 | F----IKGDGYAIGSVEGRCAIQNIDE--KN--ASQNF5FRCHRNQAGN-SAD----- | 253 | |
| yet7 | 217 | Y----NEADGYAIGSVEGRCSIRYIDDG-MQ--KKS5GFSFKCHRQTNP-N-RAPGSNGQSL | 268 | |
| | | G. S..GR .. | ..F.CHR | |
| | | VI | | |
| scBUB3 | 251 | AYPVNSIEFSPRHKFLYTAGSDGIISCWNLQTRKKIKNFAKFNE-SVVKIACSDNILCL | 309 | |
| muBUB3 | 234 | IYPVNAISFHNHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAI | 293 | |
| huBUB3 | 234 | IYPVNAISFHNHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAI | 293 | |
| rae1-hu | 273 | IYAVNGIAFHPVHGTLATVGS5DGRFSFWDKDARTKLKTSEQLDQPISACCFNHNGNIFAY | 332 | |
| rae1 | 254 | VYSVNSIAFHPQYGTFTAGSDGTF5FWDKDSHQRLKSYPNVGGTISCSTFNRTGDIFAY | 313 | |
| yet7 | 269 | VYPVNSIAFHPLYGTFTVTAGG5DGT5F5W5DKNQ5R5H5RLK5GYPTLQASIPVCSFNRNGSVFAY | 328 | |
| | | Y VN I F | T G DG W . . . | |
| scBUB3 | 310 | ATSDDTFKTNAIDQTIELNASSIYIIFDYEN----- | 341 | |
| muBUB3 | 294 | ASSYMYEMDDT-EHPE---DGIFIRQVTD5AETKPKS---T | 326 | |
| huBUB3 | 294 | ASSYMYEMDDT-EHPE---DGIFIRQVTD5AETKPKSPC-T | 328 | |
| rae1-hu | 333 | ASSYDWSKGHEFYNPQKK-NYIFL5RNA-AEELKPRNKK-- | 368 | |
| rae1 | 314 | AISYDWSKG5YTFNNAQLP-NKIMLHPVPQDEIKPRPKKGR | 352 | |
| yet7 | 329 | ALS5YDWHQGHMGNRPDYP-NVIRLHATTDEEVKEK-KK-R | 365 | |
| | | A S | E | |

Fig. 3B

Fig. 4A

| | | | | |
|----------------|---|---|---|---|
| FLAG-huBUB3 | - | - | + | + |
| huBUB3 | - | + | - | + |
| huBUB1 | + | + | + | + |
| hsMAD2 | + | + | + | + |
| α -FLAG | S | P | S | P |

*Fig. 4B*

huBUB1 (~121Kd)

FLAG-huBUB3
huBUB3 (~37Kd)

hsMAD2 (23Kd)

mRNA expression of BUB/MAD homologs in various tissues.

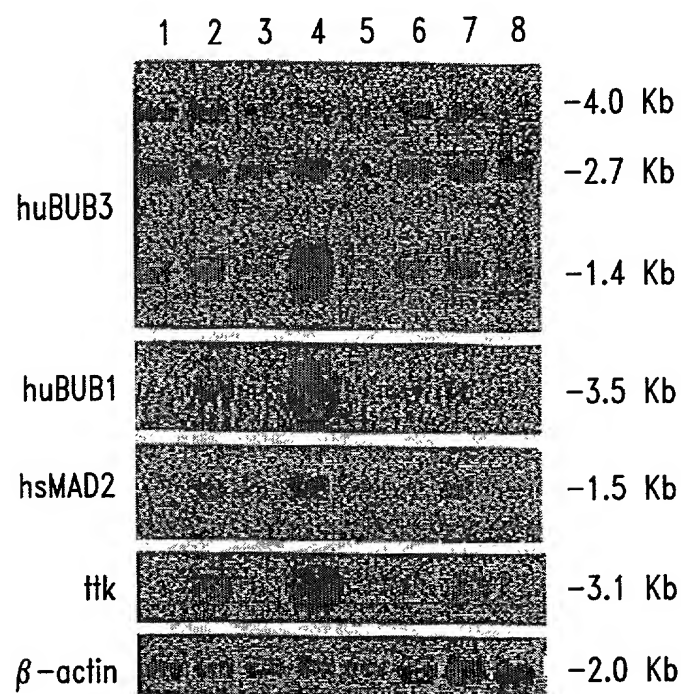


Fig. 5